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piece 1, NC\_000913, ypfJ\_purC+, config: linear, direction: +, begin: 2594730, end: 2594946

Sequence alignment diagram showing the amino acid sequence of a protein across 11 different genes. The genes are represented by colored arrows above the sequence. Amino acids are color-coded: red for aromatic (Phe, Tyr, Trp), blue for hydrophobic (Ile, Leu, Val), green for polar (Ser, Thr, Cys), yellow for acidic (Asp, Glu), purple for basic (Lys, Arg), and orange for hydroxyl (Tyr). Stop codons are marked with red dots. The sequence starts with a methionine (Met) at position 1 and ends with an arginine (Arg) at position 11.

... ] NC\_000913.ypfJ p10 3.2 bits

 p35 6.1 bits

p10 3.2 bits

 p35 6.1 bits

p10 3.2 bits

```
{-----} p35-(21)-p10 2594770 Gap 3.3 bits  
|-----| b35-p10 2594770 total 5.9 bits  
{-----} p35-(23)-p10 2594772 Gap 1.4 bits  
|-----| p35-p10 2594772 total 8.0 bits
```

----} p35-(21)-p10 2594770 Gap  
----| p35-p10 2594770 total 5.9

p35-p23)-p10 2594772 Gap 1.4 bits  
p35-p10 2594772 total 8.0 bits

p35-(23)-p10 2594772  
p35-p10 2594772 total

10. 6. 5 bit

{-----} p35-(26)-p10 2594775 Gap 3.7 bits  
p35-p10 2594775 total 8.8 bits

bio 6.

p35-(26)-p10 2594775 Gap 3.  
p35-p10 2594775 total 8 8 b

----- } p35-(26)-p10 25  
----- | p35-p10 2594775

5' \* \* 2594820 \* \* 2594830 \* \* 2594840 \* \* 2594850 \* \* 2594860 \* \* 2594870 \* \* 2594880 \* \* 2594890 3'

- glu - asp - tyr - his - arg - lys - ala - gly - - - - - fMet - ser - val - gln - cys - ile - tyr - ser - glu - ser - gly - cys - leu - ala -

- lys - ile - thr - thr - gly - lys - arg - asp - glu - met - ala - glu - glu - - - - - fMet - lys - trp - arg - arg - asp - glu - arg - ser - met - his - ile - phe - arg - glu - arg - leu - ser - cys - pro -

ir ypfJ\_purC+ ir ypfJ\_purC+ {----- ... p35-(25)-p10 2594908 Gap

---] sd-(9)-ir 2594834 Gap 2,3 bits [ #

The diagram illustrates the genomic context of the *ypfJ\_purC+* gene. It shows a blue horizontal bar representing the genome with a green vertical bar indicating the gene's location. The gene is divided into two exons: a large upper exon and a smaller lower exon. The lower exon contains five red boxes labeled '5 codons'.

```
|-----| sd-ir 2594834 ypfJ_purc+ total 7.1 bits  
  
{-----} sd-(14)-ir 2594839 Gap 4.9 bits  
-----| sd-ir 2594839 ypfJ_purc+ total 7.6 bits
```

 ... p35  
... p35  
-----  
{----- ... p35-(23)-p10 2594911 Gap  
----- ... p35-p10 2594911 total 6.  
-----

Top hit: sd-(13)-ir 2594861 Gap 4.6 bits

Bottom hit: sd-ir 2594861 ypfJ\_purC+ total 6.0 bits  
Gap 1.4 bits

Third hit: p35-(23)-p10 2594858 Gap 4.9 bits

.... p35-(25)-p10 2594908 Gap 4.0 bits <----- ... NC\_000913.purC  
.... | #####orf 27 codons  
.... | p35-p10 2594908 total 4.4 bits

